

Peaks Documentation

Module name: Peaks
Description: Determine peaks in the spectrum using a series of digital filters.
Author: D. R. Mani (Broad Institute), gp-help@broad.mit.edu
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Summary: Performs peak detection using digital convolution (moving-window) filters. The input spectrum is subjected to the following filters (in sequence): smoothing (low-pass) filter, adaptive background correction (unsharp masking) filter, and high-pass filter. The function returns a table with the original spectrum and the result of applying the filters.

References:

- D. R. Mani & Michael Gillette. 2005. *Proteomic Data Analysis: Pattern Recognition for Medical Diagnosis and Biomarker Discovery*. In Mehmed Kantardzic and Jozef Zurada (Eds.) New Generation of Data Mining Applications, IEEE Press.

Parameters:

Name	Description
spectrum.filename	spectrum data file - .csv
low.Da	Minimum M/Z to include
high.Da	Maximum M/Z to include
percentile	After applying filters, threshold above which peaks are located (default=0.65)
smoothing.size	Size of the smoothing filter (default=21)
adaptive.background.correction.strength	Strength of the adaptive background correction filter (default=0.75)
adaptive.background.correction.size	Size of the adaptive background correction filter (default=21)
high.pass.filter.strength	Strength of the high pass filter (default=10)
high.pass.filter.factor	Filter factor for the high pass filter (default=5)
output.file	output file name

Return Value:

odf file containing original spectrum and filtered (peak detected) spectrum.

Platform dependencies:

Task type: Proteomics
CPU type: any
OS: any
Language: R